



PCT

## RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/09/914,286

TIME: 10:27:44

Input Set : A:\09914286.txt

Output Set: N:\CRF3\01182002\I914286.raw

P5

3 <110> APPLICANT: OMURA, Satoshi  
4 IKEDA, Haruo  
6 <120> TITLE OF INVENTION: AVERMECTIN AGLYCON SYNTHASE GENES  
8 <130> FILE REFERENCE: 468-30/PH-775-PCT  
10 <140> CURRENT APPLICATION NUMBER: US 09/914,286  
11 <141> CURRENT FILING DATE: 2001-08-24  
13 <150> PRIOR APPLICATION NUMBER: PCT/JP00/01041  
14 <151> PRIOR FILING DATE: 2000-02-23  
16 <150> PRIOR APPLICATION NUMBER: JP 99/46961  
17 <151> PRIOR FILING DATE: 1999-02-24  
19 <160> NUMBER OF SEQ ID NOS: 16  
21 <170> SOFTWARE: PatentIn Ver. 2.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 30690  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Streptomyces avermitilis  
28 <220> FEATURE:  
30 <221> NAME/KEY: CDS  
31 <222> LOCATION: (1)..(11916)  
33 <220> FEATURE:  
35 <221> NAME/KEY: CDS  
36 <222> LOCATION: (11971)..(30687)  
38 <400> SEQUENCE: 1

ENTERED

39 gtg cag agg atg gac ggc ggg gaa gaa ccc cgc cct gcg gca ggg gag 48  
40 Val Gln Arg Met Asp Gly Gly Glu Glu Pro Arg Pro Ala Ala Gly Glu  
41 1 5 10 15  
43 gtc ctc gga gtg gcc gac gag gcg gac ggc ggc gtc gtc ttc gtt ttt 96  
44 Val Leu Gly Val Ala Asp Glu Ala Asp Gly Gly Val Val Phe Val Phe  
45 20 25 30  
47 ccc ggg cag ggc ccg caa tgg ccg ggc atg gga agg gaa ctt ctc gac 144  
48 Pro Gly Gln Gly Pro Gln Trp Pro Gly Met Gly Arg Glu Leu Leu Asp  
49 35 40 45  
51 gct tcc gac gtc ttc cgg gag agc gtc cgc gcc tgc gaa gcc gcg ttc 192  
52 Ala Ser Asp Val Phe Arg Glu Ser Val Arg Ala Cys Glu Ala Ala Phe  
53 50 55 60  
55 gcg ccc tac gtc gac tgg tcg gtg gag cag gtg ttg cgg gac tcg ccg 240  
56 Ala Pro Tyr Val Asp Trp Ser Val Glu Gln Val Leu Arg Asp Ser Pro  
57 65 70 75 80  
59 gac gct ccc ggg ctg gac cgg gtg gac gtc gtc cag ccg acc ctg ttc 288  
60 Asp Ala Pro Gly Leu Asp Arg Val Asp Val Val Gln Pro Thr Leu Phe  
61 85 90 95  
63 gcc gtc atg atc tcc ctg gcc gcc ctc tgg cgc tcg caa ggg gtc gag 336  
64 Ala Val Met Ile Ser Leu Ala Ala Leu Trp Arg Ser Gln Gly Val Glu

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65          100          105          110
67 ccg tgc gcg gtg ctg gga cac agc ctg ggc gag atc gcg gca gcc cac 384
68 Pro Cys Ala Val Leu Gly His Ser Leu Gly Glu Ile Ala Ala Ala His
69          115          120          125
71 gtc tcg gga ggc ctg tcc ctg gcc gac gcc gca cgc gtg gtg acg ctt 432
72 Val Ser Gly Gly Leu Ser Leu Ala Asp Ala Ala Arg Val Val Thr Leu
73          130          135          140
75 tgg agc cag gca cag acc acc ctt gcc ggg acc ggc gcg ctc gtc tcc 480
76 Trp Ser Gln Ala Gln Thr Thr Leu Ala Gly Thr Gly Ala Leu Val Ser
77 145          150          155          160
79 gtc gcc gcc acg ccg gat gag ctc ctg ccc cga atc gct ccg tgg acc 528
80 Val Ala Ala Thr Pro Asp Glu Leu Leu Pro Arg Ile Ala Pro Trp Thr
81          165          170          175
83 gag gac aac ccg gcg cgg ctc gcc gtc gca gcc gtc aac gga ccc cgg 576
84 Glu Asp Asn Pro Ala Arg Leu Ala Val Ala Ala Val Asn Gly Pro Arg
85          180          185          190
87 agc aca gtc gtt tcc ggt gcc cgc gag gcc gtc gcg gac ctg gtg gcc 624
88 Ser Thr Val Val Ser Gly Ala Arg Glu Ala Val Ala Asp Leu Val Ala
89          195          200          205
91 gac ctc acc gcc gcg cag gtg cgc acg cgc atg atc ccg gtg gac gtt 672
92 Asp Leu Thr Ala Ala Gln Val Arg Thr Arg Met Ile Pro Val Asp Val
93          210          215          220
95 ccc gcc cac tcc ccc ctg atg tac gcc atc gag gaa cgg gtc gtc agc 720
96 Pro Ala His Ser Pro Leu Met Tyr Ala Ile Glu Glu Arg Val Val Ser
97 225          230          235          240
99 ggc ctg ctg ccc atc acc cca cgc ccc tcc cgc atc ccc ttc cac tcc 768
100 Gly Leu Leu Pro Ile Thr Pro Arg Pro Ser Arg Ile Pro Phe His Ser
101          245          250          255
103 tcg gtg acc ggc ggc cgc ctc gac acc cgc gag cta gac gcg gcg tac 816
104 Ser Val Thr Gly Gly Arg Leu Asp Thr Arg Glu Leu Asp Ala Ala Tyr
105          260          265          270
107 tgg tac cgc aac atg tcg agc acg gtc cgg ttc gag ccc gcc gcc cgg 864
108 Trp Tyr Arg Asn Met Ser Ser Thr Val Arg Phe Glu Pro Ala Ala Arg
109          275          280          285
111 ctg ctt ctg cag cag ggg ccc aag acg ttc gtc gag atg agc ccg cac 912
112 Leu Leu Leu Gln Gln Gly Pro Lys Thr Phe Val Glu Met Ser Pro His
113          290          295          300
115 ccg gtg ctg acc atg ggc ctc cag gag ctc gcc ccg gac ctg ggc gac 960
116 Pro Val Leu Thr Met Gly Leu Gln Glu Leu Ala Pro Asp Leu Gly Asp
117 305          310          315          320
119 acc acc ggc acc gcc gac acc gtg atc atg ggc acg ctg cgc cgc gcc 1008
120 Thr Thr Gly Thr Ala Asp Thr Val Ile Met Gly Thr Leu Arg Arg Gly
121          325          330          335
123 cag ggc acc ctg gac cac ttc ctg acg tct ctc gcc caa cta cgg ggg 1056
124 Gln Gly Thr Leu Asp His Phe Leu Thr Ser Leu Ala Gln Leu Arg Gly
125          340          345          350
127 cat ggt gag acg tcg gcg acc acc gtc ctc tcg gca cgc ctg acc gcg 1104
128 His Gly Glu Thr Ser Ala Thr Thr Val Leu Ser Ala Arg Leu Thr Ala
129          355          360          365

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131	ctg	tcc	ccc	acg	cag	cag	cag	tcg	ctg	ctc	ctg	gac	ctg	gtg	cgc	gcc	1152
132	Leu	Ser	Pro	Thr	Gln	Gln	Gln	Ser	Leu	Leu	Leu	Asp	Leu	Val	Arg	Ala	
133		370					375					380					
135	cac	acc	atg	gcg	gtg	ctg	aac	gac	gac	gga	aac	gag	cgc	acc	gcg	tcg	1200
136	His	Thr	Met	Ala	Val	Leu	Asn	Asp	Asp	Gly	Asn	Glu	Arg	Thr	Ala	Ser	
137	385					390					395					400	
139	gat	gcc	ggc	cca	tcg	gcg	agt	ttc	gcc	cac	ctc	ggc	ttc	gac	tcc	gtc	1248
140	Asp	Ala	Gly	Pro	Ser	Ala	Ser	Phe	Ala	His	Leu	Gly	Phe	Asp	Ser	Val	
141					405					410					415		
143	atg	ggt	gtc	gaa	ctg	cgc	aac	cgc	ctc	agc	aag	gcc	acg	ggc	ctg	cgg	1296
144	Met	Gly	Val	Glu	Leu	Arg	Asn	Arg	Leu	Ser	Lys	Ala	Thr	Gly	Leu	Arg	
145				420					425					430			
147	ttg	ccc	gtg	acg	ctc	atc	ttc	gac	cac	acc	acg	ccg	gcc	gcg	gtc	gcc	1344
148	Leu	Pro	Val	Thr	Leu	Ile	Phe	Asp	His	Thr	Thr	Pro	Ala	Ala	Val	Ala	
149		435					440						445				
151	gcg	cgc	ctt	cgg	acc	gcg	gcg	ctc	ggc	cac	ctc	gac	gag	gac	acc	gcg	1392
152	Ala	Arg	Leu	Arg	Thr	Ala	Ala	Leu	Gly	His	Leu	Asp	Glu	Asp	Thr	Ala	
153		450					455					460					
155	ccc	gta	ccg	gac	tca	ccc	agc	ggc	cac	gga	ggc	acg	gca	gcg	gcg	gac	1440
156	Pro	Val	Pro	Asp	Ser	Pro	Ser	Gly	His	Gly	Gly	Thr	Ala	Ala	Ala	Asp	
157	465					470					475					480	
159	gac	ccg	atc	gcc	atc	atc	ggc	atg	gca	tgc	cgt	ttc	ccg	ggc	gga	gtc	1488
160	Asp	Pro	Ile	Ala	Ile	Ile	Gly	Met	Ala	Cys	Arg	Phe	Pro	Gly	Gly	Val	
161					485					490					495		
163	cgg	tcc	ccg	aag	gac	ctg	tgg	gag	ctg	gcc	gcc	tcg	ggc	gga	gac	gcc	1536
164	Arg	Ser	Pro	Lys	Asp	Leu	Trp	Glu	Leu	Ala	Ala	Ser	Gly	Gly	Asp	Ala	
165				500						505					510		
167	atc	ggg	ccg	ttc	ccc	acc	gac	cgc	gga	tgg	ccc	acg	gaa	cag	cgt	cac	1584
168	Ile	Gly	Pro	Phe	Pro	Thr	Asp	Arg	Gly	Trp	Pro	Thr	Glu	Gln	Arg	His	
169			515						520					525			
171	gcc	cag	gac	ccc	acg	cag	ccc	ggc	acg	ttc	tat	ccg	cag	gga	ggc	ggg	1632
172	Ala	Gln	Asp	Pro	Thr	Gln	Pro	Gly	Thr	Phe	Tyr	Pro	Gln	Gly	Gly	Gly	
173		530					535						540				
175	ttc	ctt	cac	gac	gcg	gcg	cac	ttc	gac	gcc	ggc	ttc	ttc	gga	atc	agt	1680
176	Phe	Leu	His	Asp	Ala	Ala	His	Phe	Asp	Ala	Gly	Phe	Phe	Gly	Ile	Ser	
177	545					550					555					560	
179	cca	cgt	gag	gca	ctg	gcg	atg	gat	ccg	cag	cag	ccg	ctg	ctg	ctg	gag	1728
180	Pro	Arg	Glu	Ala	Leu	Ala	Met	Asp	Pro	Gln	Gln	Arg	Leu	Leu	Leu	Glu	
181					565						570				575		
183	acg	tcc	tgg	gag	gcg	ttc	gag	cgg	gcg	gga	atc	gat	ccg	ctg	tcg	gta	1776
184	Thr	Ser	Trp	Glu	Ala	Phe	Glu	Arg	Ala	Gly	Ile	Asp	Pro	Leu	Ser	Val	
185				580						585					590		
187	cgc	ggg	tcc	cgt	acg	ggc	gtc	ttc	gcg	ggc	gcc	ctc	tcc	ttc	gac	tac	1824
188	Arg	Gly	Ser	Arg	Thr	Gly	Val	Phe	Ala	Gly	Ala	Leu	Ser	Phe	Asp	Tyr	
189			595				600					605					
191	ggc	ccg	cgt	atg	gac	acc	gcg	tcg	tcg	gag	ggc	gcc	gcg	gac	gtg	gag	1872
192	Gly	Pro	Arg	Met	Asp	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Ala	Asp	Val	Glu	
193		610					615					620					
195	ggc	cac	atc	ctc	acc	ggt	acc	acg	ggc	agc	gtc	ctg	tcg	ggc	cgt	atc	1920

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196 Gly His Ile Leu Thr Gly Thr Thr Gly Ser Val Leu Ser Gly Arg Ile
197 625 630 635 640
199 gcc tac agc ttc ggg ctg gaa ggg ccg gcg atc acc gtg gac acg ggg 1968
200 Ala Tyr Ser Phe Gly Leu Glu Gly Pro Ala Ile Thr Val Asp Thr Gly
201 645 650 655
203 tgc tcg gca tcg ctc gtg acg ctg cat ctg gcg tgc cag tcg ctg cgg 2016
204 Cys Ser Ala Ser Leu Val Thr Leu His Leu Ala Cys Gln Ser Leu Arg
205 660 665 670
207 tcg ggt gag tgc acg ctc gcg ctg gcc ggc ggc gtc tcg gtc atg tcc 2064
208 Ser Gly Glu Cys Thr Leu Ala Leu Ala Gly Gly Val Ser Val Met Ser
209 675 680 685
211 acc ctc ggc atg ttc atc gag ttc tcc cgg cag cgc ggg ctg tcg gtg 2112
212 Thr Leu Gly Met Phe Ile Glu Phe Ser Arg Gln Arg Gly Leu Ser Val
213 690 695 700
215 gac ggc agg tgc aag gcg tac tcg gct gca gcc gac ggc acc ggc tgg 2160
216 Asp Gly Arg Cys Lys Ala Tyr Ser Ala Ala Ala Asp Gly Thr Gly Trp
217 705 710 715 720
219 ggc gag ggc gtc ggg atg ctg ttg gtg gag cgg ttg tcg gat gcg gtg 2208
220 Gly Glu Gly Val Gly Met Leu Leu Val Glu Arg Leu Ser Asp Ala Val
221 725 730 735
223 cgg ctg ggg cat cgg gtg ctg gcg gtg gta cgc ggc agt gcg gtc aac 2256
224 Arg Leu Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn
225 740 745 750
227 cag gac ggt gcg tcg aat ggg ctg acg gcg ccg aac ggt ccg gct cag 2304
228 Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ala Gln
229 755 760 765
231 gag cgg gtg atc cgg cag gcg ttg gcg aac gcg ggg ttg tcc gtg gcg 2352
232 Glu Arg Val Ile Arg Gln Ala Leu Ala Asn Ala Gly Leu Ser Val Ala
233 770 775 780
235 gat gtg gat gtg gtg gag ggg cac ggg acg ggc acg acg ctg ggt gat 2400
236 Asp Val Asp Val Val Glu Gly His Gly Thr Gly Thr Thr Leu Gly Asp
237 785 790 795 800
239 ccg atc gag gca cag gcg ttg ctc gcc acg tac ggg cag cgg gcc ggt 2448
240 Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Gln Arg Ala Gly
241 805 810 815
243 gac agg ccg ctg tgg ctg ggg tct ctg aag tcc aac atc ggg cac acc 2496
244 Asp Arg Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr
245 820 825 830
247 atg gct gcc gcg ggt gtg ggt ggg gtc atc aag atg gtg atg gcg ttg 2544
248 Met Ala Ala Ala Gly Val Gly Gly Val Ile Lys Met Val Met Ala Leu
249 835 840 845
251 cgg gag ggg gtg ttg ccg cgg acg ttg cat gtg gat aag ccg tcg ccg 2592
252 Arg Glu Gly Val Leu Pro Arg Thr Leu His Val Asp Lys Pro Ser Pro
253 850 855 860
255 cag gtg gac tgg tcc gcg ggg gcg gtg cgg ctg ctg acg gag gcg gtg 2640
256 Gln Val Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Glu Ala Val
257 865 870 875 880
259 ccg tgg ccg ggg gac gcg gca ggg cgg ttg cgg cgg gcg gga gtg tcg 2688
260 Pro Trp Pro Gly Asp Ala Ala Gly Arg Leu Arg Arg Ala Gly Val Ser

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261		885		890		895	
263	tcg ttc ggg atc ggc ggc acg aat gcg cat gtg att ttg gag gag gcg	2736					
264	Ser Phe Gly Ile Gly Gly Thr Asn Ala His Val Ile Leu Glu Glu Ala						
265	900 905 910						
267	ccg gcg gcg ggg ggc tgt gtt gcc ggg ggt ggg gtg ttg gag ggt gct	2784					
268	Pro Ala Ala Gly Gly Cys Val Ala Gly Gly Gly Val Leu Glu Gly Ala						
269	915 920 925						
271	ccg ggt ctt gcc att tcg gtg gct gag tcg gtg gcc gct cca gtg gct	2832					
272	Pro Gly Leu Ala Ile Ser Val Ala Glu Ser Val Ala Ala Pro Val Ala						
273	930 935 940						
275	gtg tct gcg ccg gtg gct gag tcg gtg ccg gtg ccg gtg ccg gtg ccg	2880					
276	Val Ser Ala Pro Val Ala Glu Ser Val Pro Val Pro Val Pro Val Pro						
277	945 950 955 960						
279	gtt cct gtg ccg gtg tcg gct agg tct gag gct ggg ttg ccg gcg cag	2928					
280	Val Pro Val Pro Val Ser Ala Arg Ser Glu Ala Gly Leu Arg Ala Gln						
281	965 970 975						
283	gcg gag gcg ttg cgt cag tac gtg gca gtc ccg ccg gac gtt tcg ctt	2976					
284	Ala Glu Ala Leu Arg Gln Tyr Val Ala Val Arg Pro Asp Val Ser Leu						
285	980 985 990						
287	gcc gat gtg ggt gcg ggt ctg gcc tgt ggg ccg gct gtg ctg gag cat	3024					
288	Ala Asp Val Gly Ala Gly Leu Ala Cys Gly Arg Ala Val Leu Glu His						
289	995 1000 1005						
291	cgt gcg gtc gtc ctg gcc gcg gac cgt gag gag ctg gtg caa ggg ttg	3072					
292	Arg Ala Val Val Leu Ala Ala Asp Arg Glu Glu Leu Val Gln Gly Leu						
293	1010 1015 1020						
295	ggg gcg ctg gcg gcg ggt gag ccg gat ccg ccg gtg acc acg ggt cat	3120					
296	Gly Ala Leu Ala Ala Gly Glu Pro Asp Arg Arg Val Thr Thr Gly His						
297	1025 1030 1035 1040						
299	gcg ccg ggt ggt gac ccg ggc ggt gtc gtc ttc gtg ttt ccc gga cag	3168					
300	Ala Pro Gly Gly Asp Arg Gly Gly Val Val Phe Val Phe Pro Gly Gln						
301	1045 1050 1055						
303	ggt ggg cag tgg gcc ggg atg ggt gtg cgt ctg ctc gcc tcc tct ccg	3216					
304	Gly Gly Gln Trp Ala Gly Met Gly Val Arg Leu Leu Ala Ser Ser Pro						
305	1060 1065 1070						
307	gtg ttc gcc ccg ccg atg cag gcg tgc gag gag gct ctg gcg ccg tgg	3264					
308	Val Phe Ala Arg Arg Met Gln Ala Cys Glu Glu Ala Leu Ala Pro Trp						
309	1075 1080 1085						
311	gtg gac tgg tct gtg gtg gac atc ctg cgc ccg gac gcg ggg gat gcg	3312					
312	Val Asp Trp Ser Val Val Asp Ile Leu Arg Arg Asp Ala Gly Asp Ala						
313	1090 1095 1100						
315	gtg tgg gag ccg gcc gat gtg gtc cag cct gtg ctg ttc agc gtc atg	3360					
316	Val Trp Glu Arg Ala Asp Val Val Gln Pro Val Leu Phe Ser Val Met						
317	1105 1110 1115 1120						
319	gtg tct ttg gct gct ctg tgg cgt tcc tac ggt atc gaa ccc gac gcg	3408					
320	Val Ser Leu Ala Ala Leu Trp Arg Ser Tyr Gly Ile Glu Pro Asp Ala						
321	1125 1130 1135						
323	gtc ctt ggc cat tcc cag ggc gag atc gcg gcc gcg cat gtg tgt ggg	3456					
324	Val Leu Gly His Ser Gln Gly Glu Ile Ala Ala Ala His Val Cys Gly						
325	1140 1145 1150						

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\09914286.txt

Output Set: N:\CRF3\01182002\I914286.raw

L:2541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2553 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2557 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2561 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2565 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2569 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2573 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2577 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2581 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2585 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2589 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:2597 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:5125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
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L:5201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
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L:5209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:5225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:9279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:9294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:9309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15